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SEQUENCE LISTING

<110> Hauptmann, Rudolph Himmler, Adolph Maurer-Fogy, Ingrid Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for Them

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	acc Thr															240
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	cac His															336
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Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
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Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp 65 70 75 80

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Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205

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cca Pro														ggc Gly		144
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Phe	Thr 50	Ala	Ser	Glu	Asn	His 55	Leu	Arg	His	Cys	Leu 60	Ser	Cys	Ser	Lys	
Cys 65	Arg	Lys	Glu	Met	Gly 70	Gln	Val	Glu	Ile	Ser 75	Ser	Cys	Thr	Val	Asp 80	
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Ser	Glu	Asn	Leu 100	Phe	Gln	Cys	Phe	Asn 105	Cys	Ser	Leu	Cys	Leu 110	Asn	Gly	
Thr	Val	His 115	Leu	Ser	Cys	Gln	Glu 120	Lys	Gln	Asn	Thr	Val 125	Cys	Thr	Суѕ	
His	Ala 130	Gly	Phe	Phe	Leu	Arg 135	Glu	Asn	Glu	Cys	Val 140	Ser	Cys	Ser	Asn	
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						tcc Ser										336
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	cac His															336
	atc Ile															384
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His	Leu	Gly 35	Asp	Arg	Glu	Lys	Arg 40	Asp	Ser	Val	Cys	Pro 45	Gln	Gly	Lys	
Tyr	Ile 50	His	Pro	Gln	Asn	Asn 55	Ser	Ile	Cys	Cys	Thr 60	Lys	Cys	His	Lys	
Gly 65	Thr	Tyr	Leu	Tyr	Asn 70	Asp	Cys	Pro	Gly	Pro 75	Gly	Gln	Asp	Thr	Asp 80	

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Arg	His	Cys	Leu 100	Ser	Cys	Ser	Lys	Cys 105	Arg	Lys	Glu	Met	Gly 110	Gln	Val	
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Lys	Gln	Asn	Thr	Val 165	Cys	Thr	Cys	His	Ala 170	Gly	Phe	Phe	Leu	Arg 175	Glu	
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115	12	20	125	
Ser Cys Gln Glu 130	Lys Gln Asn Th	hr Val Cys Thr Cy 14	s His Ala Gly Phe O	
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Cys Pro Gly	Pro Gly G	ln Asp Thr 40	Asp Cys	Arg Glu	Cys Glu 45	Ser Gl	У
Ser Phe Thr 50	Ala Ser G	lu Asn His 55	Leu Arg	His Cys 60	Leu Ser	Cys Se	r
Lys Cys Arg 65	Lys Glu M	et Gly Gln 70	Val Glu	Ile Ser 75	Ser Cys	Thr Va	
Asp Arg Asp	Thr Val C	ys Gly Cys	Arg Lys 90	Asn Gln	Tyr Arg	His Ty 95	r
Trp Ser Glu	Asn Leu P	he Gln Cys	Phe Asn	Cys Ser	Leu Cys 110	Leu As	n
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ccc tca ggg gtt att gga ctg g Pro Ser Gly Val Ile Gly Leu V 25 30			329
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- Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205
- Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220
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Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val

65

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ctg Leu	gtc Val	att Ile	ttc Phe	ttt Phe 220	ggt Gly	ctt Leu	tgc Cys	ctt Leu	tta Leu 225	tcc Ser	ctc Leu	ctc Leu	ttc Phe	att Ile 230	ggt Gly	905
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act Thr	aag Lys 265	ccc Pro	ctg Leu	gcc Ala	cca Pro	aac Asn 270	cca Pro	agc Ser	ttc Phe	agt Ser	ccc Pro 275	act Thr	cca Pro	ggc Gly	ttc Phe	1049
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gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp 330 335 340	11
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tgaggctgcg cccctgcggg cagctctaag gaccgtcctg cgagatcgcc ttccaacccc 163	37
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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys 35 40 45									
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys 50 55 60									
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp 65 70 75 80									
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu 85 90 95									
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val									
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg									
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140									
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 145 150 155 160									
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175									
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr									
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205									
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220									
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 235 230 240									
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Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu 370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Thr Pro Arg Arg Glu Ala 405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
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Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435 440 445

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<210> 28

<211> 13

<212> PRT

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<220>

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cggctccttc acagcctcag aaaacaacaa g
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41

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42

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cleavage peptide

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probe

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	ıc aaa g .s Lys G													96
gat ac	g gac t ir Asp C	gc agg ys Arg	gag Glu	tgt Cys	gag Glu	agc Ser	ggc Gly	tcc Ser	ttc Phe	aca Thr	gcc Ala	tca Ser	gaa Glu	144

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